

**AMENDMENTS TO THE SPECIFICATION**

Please amend the specification as follows:

Change(s) applied  
to document,  
/M.C.E./  
5/13/2011

On page 9, please amend the second and third full paragraphs:

FIG. 9 is the nucleotide sequence of the wMUC-1(6) vector (SEQ ID NO: 41).

FIG. 10 is the amino acid ~~nucleotide~~-sequence of wMUC-1(6) (SEQ ID NO: 42).

On page 10, second full paragraph:

In certain embodiments the ~~nucleic acid~~ peptide molecule does not have a sequence as described in FIG. 10.

On page 10, third full paragraph:

In certain embodiments the ~~nucleic acid~~ peptide molecule has a sequence as described in FIG. 10.

On page 11, first full paragraph:

In certain embodiments the ~~nucleic acid~~ peptide molecule does not have about a 30 ~~nucleotide~~ amino acid portion of consecutive ~~nucleotides~~ amino acids of a sequence a sequence as described in FIG. 10.

On page 11, third full paragraph:

In certain embodiments the ~~nucleic acid~~ peptide molecule has a sequence as described in FIG. 10.

On page 24, first full paragraph, please amend the specification as follows:

Sequence similarity searches can be also performed manually or by using several available computer programs known to those skilled in the art. Preferably, Blast and Smith-Waterman algorithms, which are available and known to those skilled in the art, and the like can be used. Blast is NCBI's sequence similarity search tool designed to support analysis of nucleotide and protein sequence databases. The GCG Package